FIG. 1A

			·		
1	GGATAAGCCT CCTATTCGGA	GGGGCCAGCA CCCCGGTCGT	TGAGCC <u>A</u> GAG ACTCGG <u>T</u> CTC	GGAGGGAAGT CCTCCCTTCA	GACCTTCTGG
1		М	S Q R	E G S	LEDH
51	ACCAGACTGA TGGTCTGACT	CTCCTCAATC GAGGAGTTAG	TCATTCCTAC AGTAAGGATG	CCCATTTGGA GGGTAAACCT	GGCCAAGATC CCGGTTCTAG
12	Q T D	S S I	SFLP	H L E	AKI
101	CGCCAGACAC	ACAACCTTGC TGTTGGAACG	CCGCCTCCTG GGCGGAGGAC	ACCAAATATG TGGTTTATAC	CAGAACAACT GTCTTGTTGA
28	R Q T H	N L A	R L L	T K Y A	E Q L
151	TCTGGAGGAA AGACCTCCTT	ATGCACGTCG	TTGTCCCTCT	GCCCTTTGGG CGGGAAACCC	GACGGCCCGA
45	L E E	Y V Q Q	QGE	P F G	L P G F
201	TCTCACCACC AGAGTGGTGG	GCGGCTGCCG CGCCGACGGC	CTGGCCGGCC	TGAGTGGCCC ACTCACCGGG	GGCTCCGAGC CCGAGGCTCG
62	S P P	R L P	LAGL	S G P	APS
	GTACGTCCCG	ATGGCCACAG	GCTCGCCGAC	CGGCAGGATG GCCGTCCTAC	GTCGGCGGGA
				R Q D A	
301	GAGTGTGCTG CTCACACGAC	GGGCGCGACA	ACCTACGGCA	CCGCCGCCGC GGCGGCGGCG	GTCCGCCTCG
95	S V L		D A V		Q A E L
351	TGAACCCGCG ACTTGGGCGC	CGCCCCGCGC GCGGGGCGCG	CTGCTGCGGA GACGACGCCT	GCCTGGAGGA CGGACCTCCT	CGCAGCCCGC GCGTCGGGCG
112	N P R	A P R	LLRS	L E D	A A R
401	CAGGTTCGGG GTCCAAGCCC	CCCTGGGCGC GGGACCCGCG	CGCGGTGGAG GCGCCACCTC	ACAGTGCTGG TGTCACGACC	CCGCGCTGGG GGCGCGACCC
	Q V R A		A V E	T V L A	
451	CGCTGCAGCC GCGACGTCGG	CGCGGGCCCG GCGCCCGGGC	GGCCAGAGCC CCGGTCTCGG	CGTCACCGTC GCAGTGGCAG	GCCACCCTCT CGGTGGGAGA
145	A A A	R G P G	PEP	V T V	ATLF
501	TCACGGCCAA AGTGCCGGTT	CAGCACTGCA GTCGTGACGT	GGCATCTTCT CCGTAGAAGA	CAGCCAAGGT GTCGGTTCCA	CGACCCCAAG
162		S T A	G I F S		L G F
551	CACGTGTGCG GTGCACACGC	CGGAGATACC	GCTCACCCAC	AGCCGCACAG TCGGCGTGTC	TCCCGCTGGA
	H V C G			S R T E	
	CCCGGTCGAC	CACGGTCCCC	CGCAGCGGAC	AGAGTGAATA TCTCACTTAT	CTTTTTCTTG GAAAAAGAAC
195	G Q L	V P G G	V A O		

FIG. 1B

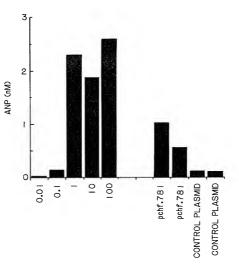
651	TAAGCTCGCT ATTCGAGCGA	CTGTCTCGCC GACAGAGCGG	TCTTTGGCTT AGAAACCGAA	CAAATTTTCT GTTTAAAAGA	GTCTCTCCAT CAGAGAGGTA
701	CTGTGTCCTG GACACAGGAC	TGTGTTCTTG ACACAAGAAC		ATCTTTCTGC TAGAAAGACG	
751	TCTCTCTCTT AGAGAGAGAA	CTGCTCTCCT GACGAGAGGA		AGCTTCTTTT TCGAAGAAAA	TTCCAACAGT AAGGTTGTCA
801	TTCTCGTTTT AAGAGCAAAA		AGTCTTGAAC TCAGAACTTG	ACTTTTGTCT TGAAAACAGA	CCGAGAGGTC GGCTCTCCAG
851	TCTTTTTGTT AGAAAAACAA	TCCTTGTCTC AGGAACAGAG		CTTTGCTTGC GAAACGAACG	TTGCTTGCTT AACGAACGAA
901	GCTTGCTTGT CGAACGAACA	TGTTGAGACA ACAACTCTGT		ATATAGCTCT TATATCGAGA	GGATGGCCTG CCTACCGGAC
951	GAACTTGCTA CTTGAACGAT	TGTAGGCCAG ACATCCGGTC	GCTGGCCTCC CGACCGGAGG	AGCTCATAGA TCGAGTATCT	GATCCACTTG CTAGGTGAAC
1001	CCTCCGACTC GGAGGCTGAG		CATCTGTCTC GTAGACAGAG	CCTGTGATCC GGACACTAGG	ATATGGGTAT TATACCCATA
1051	GTGTAACCCT CACATTGGGA	TACTTTGTCT ATGAAACAGA	CATGGAGGTG GTACCTCCAC	ACAATTTTTC TGTTAAAAAG	TCCCTTCAGT AGGGAAGTCA
1101	TTCTTTGTTC AAGAAACAAG	TTTACTGACC AAATGACTGG	AGAAAAGTGC TCTTTTCACG	CTACTTGTCC GATGAACAGG	CCTGGTGGCA GGACCACCGT
1151	AGGCCATTCA TCCGGTAAGT	CCTTAGGACC GGAATCCTGG	TTCCCACCAG AAGGGTGGTC	TTCCTTTGTA AAGGAAACAT	GGCAAATCCC CCGTTTAGGG
1201	TCCCCCTTTG AGGGGGAAAC	AGGTCCTTCC TCCAGGAAGG	CTTTCATACC GAAAGTATGG	CGGGATCCGA	GGTCAATGGA CCAGTTACCT
1251	GAGAGAAAGG CTCTCTTTCC	CAGAAAAACA GTCTTTTTGT	TCTTTAAAGA AGAAATTTCT	CAAAATAAAC	AGAATAAATT TCTTATTTAA
1301	AATTTTTGTA TTAAAAACAT		TTAACAATAA AATTGTTATT	AACTAAACTT TTGATTTGAA	
1351	AA (polyA) TT				

FIG. 2

chf.781	10 MSQREGSLEDHQTD	20 SSISFLPHLEA **	30 AKIRQTHNLAR ***		50 LEEYVQ
humontf	MAFT	EHSPLTPHRRD	LCSRSIWLAR 20	KIRSDLTAL 30	
chf.781		70 RLPLAGLSGPA	PSHAGLPVSE		
humentf	HQGLNKNINLDSAD	GMPVAST			
chf.781	110 LD-AVRRRQAELNP		130 DAARQVRALGA		GAAARG
humcntf	LARLLEDQQVHFTP		LLLQVAAFAY		
1	50 160	170	180	190	
	PGPEPVTVATLFTA		LGFHVCGLYG	EWVSRTEGD	LGQLVP
humontf	NEADGMPINV 140		WGLKVLQELS	QWTVRSIHD	
	200				
chf.781	GGVAU				

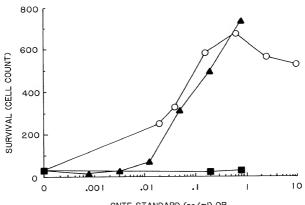
humontf SHQTGIPARGSHYIANNKKM 190 200

FIG. 3



PHENYLEPHRINE (uM) STANDARD CURVE 293 TRANSFECTION





CNTF STANDARD (ng/ml) OR
TRANSFECTED 293 CONDITIONED MEDIUM
(FRACTION OF ASSAY VOL)

FIG. 5A

1	GTGAAGGGAG CACTTCCCTC	CCGGGATCAG GGCCCTAGTC	CCAGGGGCCA GGTCCCCGGT	GCATGAGCCG CGTACTCGGC M S R	GAGGGAGGGA CTCCCTCCCT R E G
51 7	AGTCTGGAAG TCAGACCTTC S L E D	TGGGGGTCTG	ACTAAGGAGT	GTCTCACTTC CAGAGTGAAG V S L L	AAGGGGTGAA
101 24	GGAGGCCAAG CCTCCGGTTC E A K	ATCCGTCAGA TAGGCAGTCT I R Q T	${\tt GTGTGTCGGA}$	TGCGCACCTC ACGCGTGGAG A H L	CTCACCAAAT GAGTGGTTTA L T K Y
151 41	TGCGACTCGT	CGACGAGGTC	CTTATACACG	AGCTCCAGGG TCGAGGTCCC L Q G	TCTGGGGAAG
201 57	GGGCTGCCCA CCCGACGGGT G L P S	CGAAGAGCGG	CGGCGCCGAC	CCGGTGGCCG GGCCACCGGC P V A G	CGGACTCGCG
251 74		TCGGTGCGCC	CCGACGGTCA	GCACGAGCGG CGTGCTCGCC H E R	
301 91	TGCGCCGCCG	CGACCGGCGC	GACGGGGGCG	TGCTGGACGC ACGACCTGCG L D A	AGTGTGTCGC TCACACAGCG V C R
351 107		TCGACTTGGG		CGCCTGCTGC GCGGACGACG R L L R	CGGCGGACCT
401 124		GCGGTCCGGG		CGCCGCCGTG GCGGCGGCAC A A V	
451		CCCGCGGCGG	TTGGCGCCCG	CCCGGGCCGA GGGCCCGGCT R A E	CGGGGGGCGG

FIG. 5B

501 157	GCCACCGCCT CGGTGGCGGA A T A S	CAGCCGCCTC GTCGGCGGAG A A S	CGCCACCGGG GCGGTGGCCC A T G	GTCTTCCCCG CAGAAGGGGC V F P A	CCAAGGTGCT GGTTCCACGA K V L
551 174	CCCCGAGGCG	CAAACGCCGG	TCTACCGCGA AGATGGCGCT Y R E	GTGGCTGAGC CACCGACTCG W L S	CGCACCGAGG GCGTGGCTCC R T E G
601 191	GCGACCTGGG CGCTGGACCC D L G	CCAGCTGCTG GGTCGACGAC Q L L	CCCGGGGGCT GGGCCCCCGA P G G S	CGGCCTGAGC GCCGGACTCG A O	GCCGCGCGCCCG
651	AGCTCGCCCC	GCCTCCTCCC	GCTGGGTTCC	GTCTCTCCTT	CCGCTTCTTT
	TCGAGCGGGG	CGGAGGAGGG	CGACCCAAGG	CAGAGAGGAA	GGCGAAGAAA
701	GTCTTTCTCT	GCCGCTGTCG	GTGTCTGTCT	GTCTGCTCTT	AGCTGTCTCC
	CAGAAAGAGA	CGGCGACAGC	CACAGACAGA	CAGACGAGAA	TCGACAGAGG
751	ATTGCCTCGG	CCTTCTTTGC	TTTTTGTGGG	GGAGAGGGGA	GGGGACGGGC
	TAACGGAGCC	GGAAGAAACG	AAAAACACCC	CCTCTCCCCT	CCCCTGCCCG
801	AGGGTCTCTG	TCGCCCAGGC	TGGGGTGCAG	TGGCGCGATC	CCAGCACTGC
	TCCCAGAGAC	AGCGGGTCCG	ACCCCACGTC	ACCGCGCTAG	GGTCGTGACG
851	AGCCTCAACC	TCCTGGGCTC	AAGCCATCCT	TCCGCCTCAG	CTTCCCCAGC
	TCGGAGTTGG	AGGACCCGAG	TTCGGTAGGA	AGGCGGAGTC	GAAGGGGTCG
901	AGCTGGGACT	ACAGGCACGC	GCCACCACAG	CCGGCTAATT	TTTTATTTAA
	TCGACCCTGA	TGTCCGTGCG	CGGTGGTGTC	GGCCGATTAA	AAAATAAATT
951	TTTTTTGTAG	AGACGAGGTT	TCGCCATGTT	GCCCAGGCTG	GTCTTGAACT
	AAAAAACATC	TCTGCTCCAA	AGCGGTACAA	CGGGTCCGAC	CAGAACTTGA
1001	CCGGGGCTCA GGCCCCGAGT				

FIG. 6

humct1	1	MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLLIKIALQLLQLIVQLIVQL ** ***** **** * ***** * ****** **
chf.781	1	MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG
humct1		DPFGLPSFSPPRLPVAGLSAPAPSHAGLPVHERLRLDAAALAALPPLLDAVCR
chf.781	54	EPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR
humct1		RQAELNPRAPRLLRRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
chf.781	107	RQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTVAT
humct1	160	SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
chf.781	160	LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA